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RAW SEQUENCE LISTING PATENT APPLICATION US/09/543,771

DATE: 04/25/2000
TIME: 11:38:27

Input Set: I543771.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: John P. Carulli et al.
2  <120> TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
3  <130> FILE REFERENCE: 032796-013
4  <140> CURRENT APPLICATION NUMBER: US/09/543,771
5  <141> CURRENT FILING DATE: 2000-04-05
6  <150> EARLIER APPLICATION NUMBER: US 09/229,319
7  <151> EARLIER FILING DATE: 1999-01-13
8  <150> EARLIER APPLICATION NUMBER: US 60/071,449
9  <151> EARLIER FILING DATE: 1998-01-13
10 <150> EARLIER APPLICATION NUMBER: US 60/105,511
11 <151> EARLIER FILING DATE: 1998-10-23
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13 <210> SEQ ID NO 1
14 <211> LENGTH: 5120
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
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19 gccggacaac atg gag gca gcg ccg ggg ccg ccg tgg ccg ctg ctg      109
20 Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
21      1              5              10
22 ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc      157
23 Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
24      15              20              25
25 gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc cgg gac gta cgg ctg      205
26 Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
27      30              35              40              45
28 gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc      253
29 Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
30      50              55              60
31 ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg      301
32 Leu Glu Asp Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
33      65              70              75
34 tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac      349
35 Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
36      80              85              90
37 cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc gcc ctg gtc tct      397
38 Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
39      95              100              105
40 ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg      445
41 Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr
42      110              115              120              125
43 gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc      493
44 Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser

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47	Arg	Lys	Val	Leu	Phe	Trp	Gln	Asp	Leu	Asp	Gln	Pro	Arg	Ala	Ile	Ala	
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49	ttg	gac	ccc	gct	cac	ggg	tac	atg	tac	tgg	aca	gac	tgg	ggt	gag	acg	589
50	Leu	Asp	Pro	Ala	His	Gly	Tyr	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Glu	Thr	
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53	Pro	Arg	Ile	Glu	Arg	Ala	Gly	Met	Asp	Gly	Ser	Thr	Arg	Lys	Ile	Ile	
54		175					180				185						
55	gtg	gac	tcg	gac	att	tac	tgg	ccc	aat	gga	ctg	acc	atc	gac	ctg	gag	685
56	Val	Asp	Ser	Asp	Ile	Tyr	Trp	Pro	Asn	Gly	Leu	Thr	Ile	Asp	Leu	Glu	
57	190					195				200					205		
58	gag	cag	aag	ctc	tac	tgg	gct	gac	gcc	aag	ctc	agc	ttc	atc	cac	cgt	733
59	Glu	Gln	Lys	Leu	Tyr	Trp	Ala	Asp	Ala	Lys	Leu	Ser	Phe	Ile	His	Arg	
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61	gcc	aac	ctg	gac	ggc	tcg	ttc	cgg	cag	aag	gtg	gtg	gag	ggc	agc	ctg	781
62	Ala	Asn	Leu	Asp	Gly	Ser	Phe	Arg	Gln	Lys	Val	Val	Glu	Gly	Ser	Leu	
63			225				230				235						
64	acg	cac	ccc	ttc	gcc	ctg	acg	ctc	tcc	ggg	gac	act	ctg	tac	tgg	aca	829
65	Thr	His	Pro	Phe	Ala	Leu	Thr	Leu	Ser	Gly	Asp	Thr	Leu	Tyr	Trp	Thr	
66		240				245				250							
67	gac	tgg	cag	acc	cgc	tcc	atc	cat	gcc	tgc	aac	aag	cgc	act	ggg	ggg	877
68	Asp	Trp	Gln	Thr	Arg	Ser	Ile	His	Ala	Cys	Asn	Lys	Arg	Thr	Gly	Gly	
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70	aag	agg	aag	gag	atc	ctg	agt	gcc	ctc	tac	tca	ccc	atg	gac	atc	cag	925
71	Lys	Arg	Lys	Glu	Ile	Leu	Ser	Ala	Leu	Tyr	Ser	Pro	Met	Asp	Ile	Gln	
72	270					275				280					285		
73	gtg	ctg	agc	cag	gag	cgg	cag	cct	ttc	ttc	cac	act	cgc	tgt	gag	gag	973
74	Val	Leu	Ser	Gln	Glu	Arg	Gln	Pro	Phe	Phe	His	Thr	Arg	Cys	Glu	Glu	
75				290				295					300				
76	gac	aat	ggc	ggc	tgc	tcc	cac	ctg	tgc	ctg	ctg	tcc	cca	agc	gag	cct	1021
77	Asp	Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Leu	Leu	Ser	Pro	Ser	Glu	Pro	
78			305				310					315					
79	ttc	tac	aca	tgc	gcc	tgc	ccc	acg	ggt	gtg	cag	ctg	cag	gac	aac	ggc	1069
80	Phe	Tyr	Thr	Cys	Ala	Cys	Pro	Thr	Gly	Val	Gln	Leu	Gln	Asp	Asn	Gly	
81			320				325					330					
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95	Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr	
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97	gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac	1357
98	Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn	
99	415 420 425	
100	ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc	1405
101	Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu	
102	430 435 440 445	
103	aac ggc acc tcc cgc aag atc ctg gtg tcg gag gac ctg gac gag ccc	1453
104	Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro	
105	450 455 460	
106	cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac	1501
107	Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp	
108	465 470 475	
109	tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag	1549
110	Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu	
111	480 485 490	
112	cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc	1597
113	Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala	
114	495 500 505	
115	ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac	1645
116	Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp	
117	510 515 520 525	
118	aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg	1693
119	Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu	
120	530 535 540	
121	gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc	1741
122	Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe	
123	545 550 555	
124	atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag	1789
125	Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys	
126	560 565 570	
127	gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg	1837
128	Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met	
129	575 580 585	
130	ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt	1885
131	Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys	
132	590 595 600 605	
133	gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac	1933
134	Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His	
135	610 615 620	
136	gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg	1981
137	Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met	
138	625 630 635	
139	aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc	2029
140	Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala	
141	640 645 650	
142	gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc	2077
143	Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile	
144	655 660 665	

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146	Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser	
147	670 675 680 685	
148	aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc	2173
149	Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg	
150	690 695 700	
151	gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt	2221
152	Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu	
153	705 710 715	
154	gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac	2269
155	Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr	
156	720 725 730	
157	tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg	2317
158	Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly	
159	735 740 745	
160	cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg	2365
161	Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser	
162	750 755 760 765	
163	ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc	2413
164	Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly	
165	770 775 780	
166	ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg	2461
167	Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met	
168	785 790 795	
169	acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac	2509
170	Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr	
171	800 805 810	
172	gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag	2557
173	Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu	
174	815 820 825	
175	tcg tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc	2605
176	Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu	
177	830 835 840 845	
178	ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca	2653
179	Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr	
180	850 855 860	
181	gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg	2701
182	Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg	
183	865 870 875	
184	aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg	2749
185	Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu	
186	880 885 890	
187	gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac	2797
188	Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn	
189	895 900 905	
190	aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc	2845
191	Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg	
192	910 915 920 925	
193	tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc	2893
194	Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys	

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196	agc ccg ccc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt							2941
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198		945		950		955		
199	cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg							2989
200	Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu							
201		960		965		970		
202	cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag							3037
203	His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys							
204		975		980		985		
205	ttc atc tac tgg gtg gat ggg cgc cag aac atc aag cga gcc aag gac							3085
206	Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp							
207	990		995		1000		1005	
208	gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac							3133
209	Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn							
210		1010		1015		1020		
211	cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca							3181
212	Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr							
213		1025		1030		1035		
214	ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg							3229
215	Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu							
216		1040		1045		1050		
217	agc ggg gaa gcc atg ggg gtg ctg cgt ggg gac cgc gac aag ccc							3277
218	Ser Gly Glu Ala Met Gly Val Leu Arg Gly Asp Arg Asp Lys Pro							
219		1055		1060		1065		
220	agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac							3325
221	Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn							
222		1070		1075		1080		1085
223	atg cag gac cgg gca gcc aag atc gaa cgc gca gcc ctg gac ggc acc							3373
224	Met Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr							
225		1090		1095		1100		
226	gag cgc gag gtc ctc ttc acc acc ggc ctc atc cgc cct gtg gcc ctg							3421
227	Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu							
228		1105		1110		1115		
229	gtg gtg gac aac aca ctg ggc aag ctg ttc tgg gtg gac gcg gac ctg							3469
230	Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu							
231		1120		1125		1130		
232	aag cgc att gag agc tgt gac ctg tca ggg gcc aac cgc ctg acc ctg							3517
233	Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu							
234		1135		1140		1145		
235	gag gac gcc aac atc gtg cag cct ctg ggc ctg acc atc ctt ggc aag							3565
236	Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys							
237		1150		1155		1160		1165
238	cat ctc tac tgg atc gac cgc cag cag cag atg atc gag cgt gtg gag							3613
239	His Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu							
240		1170		1175		1180		
241	aag acc acc ggg gac aag cgg act cgc atc cag ggc cgt gtc gcc cac							3661
242	Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His							
243		1185		1190		1195		
244	ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca							3709

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I543771.RAW

Line	?	Error/Warning	Original Text
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1331	W	"N" or "Xaa" used: Feature required	tccgtttcna aaaacaaaca aacaaacaaa taaacaaa
1563	W	"N" or "Xaa" used: Feature required	gcatgtgcct gtaatcccag ctacttagga ggnnnnct
1653	W	"N" or "Xaa" used: Feature required	gaagacctgg ctgtangtgg ggtangcang ctttctaa
1654	W	"N" or "Xaa" used: Feature required	tggagtggc angtttccga aaagaagaaa agctgact
1655	W	"N" or "Xaa" used: Feature required	ggaacangca ggcttcttgg aagaagaaaa tctggctg
2643	W	"N" or "Xaa" used: Feature required	ctggccaaga ctggcacena gctacacana aagtatan
2792	W	"N" or "Xaa" used: Feature required	gcgtagaaag ccctgnaaac tggagggagc cctttgtc
3296	W	"N" or "Xaa" used: Feature required	ctttnttttt tttttttttt tttttttttt tttgaaat